

SEQUENCE LISTING

<110> Xia, Zhi-Qiang
Costa, Michael A
Davlin, Laurence B
Lewis, Norman G

<120> Recombinant Secoisolariciresinol Dehydrogenase, and
methods of Use

<130> wsur113787

<140> Not yet assigned

<141> 1999-04-23

<150> 60/082,977

<151> 1998-04-24

<160> 25

<170> PatentIn Ver. 2.0

<210> 1

<211> 819

<212> DNA

<213> Forsythia x intermedia

<220>

<221> CDS

<222> (1)..(819)

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Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu	
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ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa	144
Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu	
35 40 45	
tta ggt cac tca gtt gtc gag gcc att ggc act tcc aat tcc acc tac	192
Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr	
50 55 60	
atc cac tgt gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac	240
Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp	
65 70 75 80	
aac aca gtt tca acc tat gga aaa ctg gac att atg ttc agc aat gca	288
Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala	
85 90 95	
gga att tct gat ccc aac agg ccc cgc atc ata gac aac gaa aaa gca	336
Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala	
100 105 110	

100	105	110	
gac ttt gaa cgc gtt ctc agt gta aat gta acc gga gtt ttc cta tgc			384
Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys			
115	120	125	
atg aag cac gca gca cgt gtt atg att cca gca cgc agt ggc aac ata			432
Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile			
130	135	140	
att tcc act gct agt tta agc tca act atg ggt ggt ggt tct tca cat			480
Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His			
145	150	155	160
gcc tat tgt ggt tca aag cat gct gtg tta gcc ctt act agg aat ctg			528
Ala Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu			
165	170	175	
gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct			576
Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro			
180	185	190	
ttc ggg ctt cct acg gct tta ggc aag aaa ttt tca ggg att aaa aat			624
Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn			
195	200	205	
gaa gaa gaa ttt gag aat gta ata aac ttt gcg gga aat ttg aaa ggt			672
Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly			
210	215	220	
cca aaa ttt aat gtt gag gat gtt gcc aat gca gct ctt tat ctg gct			720
Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala			
225	230	235	240
agt gat gag gca aaa tac gtg agt gga cac aat ctg ttc att gat gga			768
Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly			
245	250	255	
ggg ttc agc gtc tgc aat tct gta atc aaa gtg ttc caa tat cca gat			816
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tct			819
Ser			

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<212> PRT

<213> Forsythia x intermedia

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			20					25					30		

Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu
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 Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr
 50 55 60
 Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp
 65 70 75 80
 Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala
 85 90 95
 Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala
 100 105 110
 Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys
 115 120 125
 Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile
 130 135 140
 Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His
 145 150 155 160
 Ala Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu
 165 170 175
 Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro
 180 185 190
 Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn
 195 200 205
 Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly
 210 215 220
 Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala
 225 230 235 240
 Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly
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 Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp
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 Ser

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 <213> Forsythia x intermedia

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Gly Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr
                20                25                30

aca gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat 144
Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp
                35                40                45

gtc caa gat gaa tta ggt cac tca gtt gtc gag gcc att ggc act tcc 192
Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser
                50                55                60

aat tcc acc tac atc cac tgt gat gtt act aat gaa gac ggt gtt aaa 240
Asn Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys
        65                70                75                80

aat gcc gtg gac aac aca gtt tca acc tat gga aaa ctg gac att atg 288
Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met
                85                90                95

ttc agc aat gca gga att tct gat ccc aac agg ccc cgc atc ata gac 336
Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp
                100                105                110

aac gaa aaa gca gac ttt gaa cgc gtt ttc agt gta aat gta acc gga 384
Asn Glu Lys Ala Asp Phe Glu Arg Val Phe Ser Val Asn Val Thr Gly
                115                120                125

gtt ttc cta tgc atg aag cac gca gca cgt gtt atg att cca gca cgc 432
Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg
                130                135                140

agt ggc aac ata att tcc act gct agt tta agc tca act atg ggt ggt 480
Ser Gly Asn Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly
        145                150                155                160

ggt tct tca cat gcc tat tgt ggt tca aag cat gct gtg tta ggc ctt 528
Gly Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu
                165                170                175

act agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat 576
Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn
                180                185                190

tgt ttg tct cct ttc ggg ctt cct acg gct tta ggc aag aaa ttt tca 624
Cys Leu Ser Pro Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser
                195                200                205

ggg att aaa aat gaa gaa gaa ttt gag aat gta ata aac ttt gcg gga 672
Gly Ile Lys Asn Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly
        210                215                220

aat ctg aaa ggt cca aaa ttt aat gtt gag gat gtt gcc aat gca gct 720

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Asn Leu Lys Gly Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala
 225 230 235 240
 ctt tat ctg gct agt gat gag gca aaa tac gtg agt gga cac aat ctg 768
 Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu
 245 250 255
 ttc att gat gga ggg ttc agc gtc tgc aat tct gta atc aaa gtg ttc 816
 Phe Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe
 260 265 270
 caa tat cca gat tct 831
 Gln Tyr Pro Asp Ser
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<210> 4
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 <212> PRT
 <213> Forsythia x intermedia

<400> 4
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 Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp
 35 40 45
 Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser
 50 55 60
 Asn Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys
 65 70 75 80
 Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met
 85 90 95
 Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp
 100 105 110
 Asn Glu Lys Ala Asp Phe Glu Arg Val Phe Ser Val Asn Val Thr Gly
 115 120 125
 Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg
 130 135 140
 Ser Gly Asn Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly
 145 150 155 160
 Gly Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu
 165 170 175
 Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn
 180 185 190

Cys Leu Ser Pro Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser
 195 200 205
 Gly Ile Lys Asn Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly
 210 215 220
 Asn Leu Lys Gly Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala
 225 230 235 240
 Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu
 245 250 255
 Phe Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe
 260 265 270
 Gln Tyr Pro Asp Ser
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<220>
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 <222> (1)..(819)

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 Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr Ala Lys Leu
 20 25 30
 ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa 144
 Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu
 35 40 45
 tta ggt cac tca gtt gtc gag gcc att ggc cct tcc aat tcc acc tac 192
 Leu Gly His Ser Val Val Glu Ala Ile Gly Pro Ser Asn Ser Thr Tyr
 50 55 60
 atc cac tgc gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac 240
 Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp
 65 70 75 80
 aac aca gtt tca acc tat gga aaa ctg gac att atg ttc aac aat gca 288
 Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Asn Asn Ala
 85 90 95
 gga att tct gat ccc tac aag ccc cgg gtc ata gac aac gaa aaa gca 336
 Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn Glu Lys Ala
 100 105 110
 gac ttt gaa cgc gtt ctc agt gtn aat gtn acc gga gtt ttc cta ttt 384

Asp Phe Glu Arg Val Leu Ser Xaa Asn Xaa Thr Gly Val Phe Leu Phe
 115 120 125
 atg aag cac gca gca cgc att atg gtt cca gca cga aat ggc tgc ata 432
 Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Asn Gly Cys Ile
 130 135 140
 att tcc act gct agt tta agc tca act atg ggt ggt ggt tct tca cat 480
 Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Ser Ser His
 145 150 155 160
 gct tat tgt ggt gca aaa cat gct gta tta ggc ctt act agg aat ctg 528
 Ala Tyr Cys Gly Ala Lys His Ala Val Leu Gly Leu Thr Arg Asn Leu
 165 170 175
 gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct 576
 Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro
 180 185 190
 ttc ggg ctt cct acg cct cta gcc aag aaa ttt tca ggg att gaa aat 624
 Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Ser Gly Ile Glu Asn
 195 200 205
 gat gta gac ttt gcg aat gca ata gaa cat gcg gga aat ctg aaa ggt 672
 Asp Val Asp Phe Ala Asn Ala Ile Glu His Ala Gly Asn Leu Lys Gly
 210 215 220
 aca aaa ttg agg att gag gat gtt gcc aat gca gct ctt ttt ctg gct 720
 Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu Phe Leu Ala
 225 230 235 240
 agt gat gag gca caa tat gtg agt gga caa aat ctg ttc atc gat gga 768
 Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe Ile Asp Gly
 245 250 255
 ggg ttc agc gtc tgc aat tct gca atc aaa atg ttc caa tat cca gac 816
 Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Met Phe Gln Tyr Pro Asp
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 tct 819
 Ser

<210> 6

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<212> PRT

<213> Forsythia x intermedia

<400> 6

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 35 40 45

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 Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp
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 85 90 95
 Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn Glu Lys Ala
 100 105 110
 Asp Phe Glu Arg Val Leu Ser Xaa Asn Xaa Thr Gly Val Phe Leu Phe
 115 120 125
 Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Asn Gly Cys Ile
 130 135 140
 Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His
 145 150 155 160
 Ala Tyr Cys Gly Ala Lys His Ala Val Leu Gly Leu Thr Arg Asn Leu
 165 170 175
 Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro
 180 185 190
 Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Ser Gly Ile Glu Asn
 195 200 205
 Asp Val Asp Phe Ala Asn Ala Ile Glu His Ala Gly Asn Leu Lys Gly
 210 215 220
 Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu Phe Leu Ala
 225 230 235 240
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 245 250 255
 Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Met Phe Gln Tyr Pro Asp
 260 265 270

Ser

<210> 7
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 <213> Forsythia x intermedia

<220>
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gga aaa gtt gcc ctt ata aca gga gga gcc agt gga att gga gaa ttc				96
Gly Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Phe	20	25	30	
aca gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat				144
Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp	35	40	45	
gtc caa gat gaa tta ggt cac tca gtt gtc gag gcc atc ggc act tcc				192
Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser	50	55	60	
aat tcc atc tac atc cac tgc gat gtt acc aat gaa gac gat gtt aaa				240
Asn Ser Ile Tyr Ile His Cys Asp Val Thr Asn Glu Asp Asp Val Lys	65	70	75	80
aat gcc gtg gac aac aca gtt tca acc tat gga aaa ctg gac att atg				288
Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met	85	90	95	
ttc aac aat gca gga att gct gac ccc aac aag ccc cgc atc gta gac				336
Phe Asn Asn Ala Gly Ile Ala Asp Pro Asn Lys Pro Arg Ile Val Asp	100	105	110	
aac gaa aaa gca gac ttt gaa cgc gtt ctc agc gta aat gta acc ggt				384
Asn Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly	115	120	125	
gtt ttc cta tgc atg aag cac gca gca cgc gtt atg gtg cca gca cgc				432
Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Val Pro Ala Arg	130	135	140	
agt ggc agc ata att tcc act gct agc gta agc tca aca att ggt ggt				480
Ser Gly Ser Ile Ile Ser Thr Ala Ser Val Ser Ser Thr Ile Gly Gly	145	150	155	160
gct gct tca cat gct tat tgt tgt tca aag cat gct gtg tta ggc ctt				528
Ala Ala Ser His Ala Tyr Cys Cys Ser Lys His Ala Val Leu Gly Leu	165	170	175	
act agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat				576
Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn	180	185	190	
tgt ttg gct cct tac gcg ctt gct acg cct tta gcc aag aaa ttt gta				624
Cys Leu Ala Pro Tyr Ala Leu Ala Thr Pro Leu Ala Lys Lys Phe Val	195	200	205	
ggg ctt gaa aat gac gaa gat ttg gag aat gca atg agc ctt atg gga				672
Gly Leu Glu Asn Asp Glu Asp Leu Glu Asn Ala Met Ser Leu Met Gly	210	215	220	
aat ctg aaa ggt aca aat ttg aag gct gag gac gtc gcc aat gca gct				720
Asn Leu Lys Gly Thr Asn Leu Lys Ala Glu Asp Val Ala Asn Ala Ala	225	230	235	240

-10-

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 Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu
 245 250 255
 ttc att gat gga ggg ttc agc gtc tac aat tct gca atc aaa atg ttc 816
 Phe Ile Asp Gly Gly Phe Ser Val Tyr Asn Ser Ala Ile Lys Met Phe
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 Gln Tyr Pro Asp Thr
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<210> 8
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 <213> Forsythia x intermedia

<400> 8
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 35 40 45
 Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser
 50 55 60
 Asn Ser Ile Tyr Ile His Cys Asp Val Thr Asn Glu Asp Asp Val Lys
 65 70 75 80
 Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met
 85 90 95
 Phe Asn Asn Ala Gly Ile Ala Asp Pro Asn Lys Pro Arg Ile Val Asp
 100 105 110
 Asn Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly
 115 120 125
 Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Val Pro Ala Arg
 130 135 140
 Ser Gly Ser Ile Ile Ser Thr Ala Ser Val Ser Ser Thr Ile Gly Gly
 145 150 155 160
 Ala Ala Ser His Ala Tyr Cys Cys Ser Lys His Ala Val Leu Gly Leu
 165 170 175
 Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn
 180 185 190
 Cys Leu Ala Pro Tyr Ala Leu Ala Thr Pro Leu Ala Lys Lys Phe Val
 195 200 205

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Gly Leu Glu Asn Asp Glu Asp Leu Glu Asn Ala Met Ser Leu Met Gly
 210 215 220

Asn Leu Lys Gly Thr Asn Leu Lys Ala Glu Asp Val Ala Asn Ala Ala
 225 230 235 240

Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu
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Gln Tyr Pro Asp Thr
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 Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr
 20 25 30

gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc 144
 Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val
 35 40 45

caa gat gaa tta ggt cac tca gtt gtc gag gcc att ggc ctt tcc aat 192
 Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Leu Ser Asn
 50 55 60

tcc acc tac atc cac tgc gat gtt act aat gaa gac ggt gtt aaa aat 240
 Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn
 65 70 75 80

gcc gtg gac aac aca gtt tca acc tat gga aaa ctg gac att atg ttc 288
 Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe
 85 90 95

aac aat gca gga att tct gat ccc tac aag ccc cgg gtc ata gac aac 336
 Asn Asn Ala Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn
 100 105 110

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 Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val
 115 120 125

ttc cta ttt atg aag cac gca gca cgc att atg gtt cca gca cga agt 432
 Phe Leu Phe Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Ser
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 Gly Cys Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly
 145 150 155 160
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 Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu Thr
 165 170 175
 agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt 576
 Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys
 180 185 190
 ttg tct cct ttc ggg ctt cct acg cct tta gcc aag aaa ttt aca ggg 624
 Leu Ser Pro Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Thr Gly
 195 200 205
 att gaa aat gat gaa gac ttg gcg aat gga ata gaa cgt gcg gga aat 672
 Ile Glu Asn Asp Glu Asp Leu Ala Asn Gly Ile Glu Arg Ala Gly Asn
 210 215 220
 ctg aaa ggt aca aaa ttg agg att gag gat gtt gcc aat gca gct ctt 720
 Leu Lys Gly Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu
 225 230 235 240
 ttt ctg gct agt gat gag gca caa tat gtg agt gga caa aat ctg ttc 768
 Phe Leu Ala Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe
 245 250 255
 atc gat gga ggg ttc agc gtc tgc aat tct gca atc aaa ttg ttc caa 816
 Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Leu Phe Gln
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 tat cca gac tct 828
 Tyr Pro Asp Ser
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<210> 10

<211> 276

<212> PRT

<213> Forsythia x intermedia

<400> 10

Met Ala Thr Ser Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly
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Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr
 20 25 30

Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val
 35 40 45

Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Leu Ser Asn
 50 55 60

-13-

Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn
 65 70 75 80
 Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe
 85 90 95
 Asn Asn Ala Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn
 100 105 110
 Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val
 115 120 125
 Phe Leu Phe Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Ser
 130 135 140
 Gly Cys Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly
 145 150 155 160
 Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu Thr
 165 170 175
 Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys
 180 185 190
 Leu Ser Pro Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Thr Gly
 195 200 205
 Ile Glu Asn Asp Glu Asp Leu Ala Asn Gly Ile Glu Arg Ala Gly Asn
 210 215 220
 Leu Lys Gly Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu
 225 230 235 240
 Phe Leu Ala Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe
 245 250 255
 Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Leu Phe Gln
 260 265 270
 Tyr Pro Asp Ser
 275

<210> 11
 <211> 21
 <212> PRT
 <213> Forsythia x intermedia

<220>
 <221> PEPTIDE
 <222> (1)..(21)
 <223> N-terminal peptide of F. intermedia
 secoisolariciresinol protein wherein Xaa at
 positions 3, 12 and 20 represents an unidentified
 amino acid residue

<400> 11

-14-

Gln Val Xaa Thr Ala Ile Ala Arg Asp Leu Glu Xaa Lys Val Ala Leu
 1 5 10 15

Ile Thr Gly Xaa Ala
 20

<210> 12
 <211> 17
 <212> PRT
 <213> Forsythia x intermedia

<400> 12
 Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala
 1 5 10 15

Lys

<210> 13
 <211> 15
 <212> PRT
 <213> Forsythia x intermedia

<400> 13
 Leu Asn Ile Met Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Lys
 1 5 10 15

<210> 14
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<220>
 <221> misc_feature
 <222> (1)..(20)
 <223> PCR primer wherein n at positions 3, 9, 15 and 18
 represents inosine

<400> 14
 ggnathggng aracnacngc

20

<210> 15
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer wherein n at positions 3 and 9
represents inosine

<400> 15
ccngcrttng araacatdat

20

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer wherein n at positions 3 and 9
represents inosine

<400> 16
ccngcrttnc traacatdat

20

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer

<400> 17
attccgctag attgcattga

20

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature

<222> (1)..(20)
<223> PCR primer wherein n at positions 3 and 9
represent inosine

<400> 18
ccngcrttnc traacatdat

20

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> T7 PCR primer

<400> 19
aattaaccct cactaaaggg

20

<210> 20
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(23)
<223> PCR primer

<400> 20
cagcttcgaa ctgcattcgc aag

23

<210> 21
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(22)
<223> T7 PCR primer

<400> 21
cgggatatca ctcagcataa tg

22

<210> 22
<211> 816
<212> DNA
<213> Forsythia x intermedia

<220>
<221> CDS
<222> (1)..(816)

<400> 22
cag ctt cga act gca ttc gca aga agg cta gaa gga aaa gtt gcc ctt 48
Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala Leu
1 5 10 15
ata aca gga gga gcc agt gga att gga gaa acc aca gca aaa ctc ttc 96
Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu Phe
20 25 30
tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa tta 144
Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu Leu
35 40 45
ggg cac tca gtt gtc gag gcc att ggc act tcc aat tcc acc tac atc 192
Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr Ile
50 55 60
cac tgt gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac aac 240
His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp Asn
65 70 75 80
aca gtt tca acc tat gga aaa ctg gac att atg ttc agc aat gca gga 288
Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala Gly
85 90 95
att tct gat ccc aac agg ccc cgc atc ata gac aac gaa aaa gca gac 336
Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala Asp
100 105 110
ttt gaa cgc gtt ctc agt gta aat gta acc gga gtt ttc cta tgc atg 384
Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys Met
115 120 125
aag cac gca gca cgt gtt atg att cca gca cgc agt ggc aac ata att 432
Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile Ile
130 135 140
tcc act gct agt tta agc tca act atg ggt ggt ggt tct tca cat gcc 480
Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His Ala
145 150 155 160
tat tgt ggt tca aag cat gct gtg tta gcc ctt act agg aat ctg gca 528
Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu Ala
165 170 175

gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct ttc 576
 Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro Phe
 180 185 190

ggg ctt cct acg gct tta ggc aag aaa ttt tca ggg att aaa aat gaa 624
 Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn Glu
 195 200 205

gaa gaa ttt gag aat gta ata aac ttt gcg gga aat ttg aaa ggt cca 672
 Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly Pro
 210 215 220

aaa ttt aat gtt gag gat gtt gcc aat gca gct ctt tat ctg gct agt 720
 Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala Ser
 225 230 235 240

gat gag gca aaa tac gtg agt gga cac aat ctg ttc att gat gga ggg 768
 Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly Gly
 245 250 255

ttc agc gtc tgc aat tct gta atc aaa gtg ttc caa tat cca gat tct 816
 Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp Ser
 260 265 270

<210> 23

<211> 272

<212> PRT

<213> Forsythia x intermedia

<400> 23

Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala Leu
 1 5 10 15

Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu Phe
 20 25 30

Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu Leu
 35 40 45

Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr Ile
 50 55 60

His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp Asn
 65 70 75 80

Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala Gly
 85 90 95

Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala Asp
 100 105 110

Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys Met
 115 120 125

Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile Ile
 130 135 140

Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His Ala
 145 150 155 160
 Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu Ala
 165 170 175
 Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro Phe
 180 185 190
 Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn Glu
 195 200 205
 Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly Pro
 210 215 220
 Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala Ser
 225 230 235 240
 Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly Gly
 245 250 255
 Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp Ser
 260 265 270

<210> 24
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<220>
 <221> misc_feature
 <222> (1)..(33)
 <223> PCR primer

<400> 24
 acatatgcag cttcgaaactg cattcgcaag aag

33

<210> 25
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<220>
 <221> misc_feature
 <222> (1)..(33)
 <223> PCR primer

<400> 25

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catatgggca gacatgttac atgatcaatt gca

33